

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:13:58 ; Search time 101.503 Seconds
(without alignments)
2360.331 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|----------|--------------------|
| 1 | 2789 | 100.0 | 524 | 2 | AAR70783 | Aar70783 Prosaposi |
| 2 | 2789 | 100.0 | 524 | 2 | AAW85652 | Aaw85652 Human pro |
| 3 | 2789 | 100.0 | 524 | 3 | AAY58716 | Aay58716 Human pro |
| 4 | 2789 | 100.0 | 524 | 6 | ABU79099 | Abu79099 Lip-TAA b |
| 5 | 2789 | 100.0 | 524 | 6 | ABU05200 | Abu05200 Human exp |
| 6 | 2789 | 100.0 | 524 | 6 | ABU05207 | Abu05207 Human exp |
| 7 | 2789 | 100.0 | 524 | 6 | ABU05203 | Abu05203 Human exp |
| 8 | 2789 | 100.0 | 524 | 6 | ABU07340 | Abu07340 Human exp |
| 9 | 2789 | 100.0 | 524 | 6 | ABU05216 | Abu05216 Human exp |
| 10 | 2789 | 100.0 | 524 | 6 | ABU05202 | Abu05202 Human exp |
| 11 | 2789 | 100.0 | 524 | 6 | ABU05214 | Abu05214 Human exp |
| 12 | 2789 | 100.0 | 524 | 6 | ABU05215 | Abu05215 Human exp |
| 13 | 2789 | 100.0 | 524 | 6 | ABU05199 | Abu05199 Human exp |
| 14 | 2789 | 100.0 | 524 | 6 | ABU05212 | Abu05212 Human exp |
| 15 | 2789 | 100.0 | 524 | 6 | ABU05213 | Abu05213 Human exp |
| 16 | 2789 | 100.0 | 524 | 6 | ABU05205 | Abu05205 Human exp |

| | | | | | | | |
|----|--------|-------|-----|---|----------|----------|-----------|
| 17 | 2789 | 100.0 | 524 | 7 | ADF43340 | Adf43340 | Superanti |
| 18 | 2789 | 100.0 | 524 | 7 | ADJ69401 | Adj69401 | Human hea |
| 19 | 2789 | 100.0 | 524 | 8 | ADO08060 | Ado08060 | Human pol |
| 20 | 2789 | 100.0 | 524 | 8 | ADQ94328 | Adq94328 | Human Pre |
| 21 | 2789 | 100.0 | 524 | 8 | ABM81149 | Abm81149 | Tumour-as |
| 22 | 2789 | 100.0 | 524 | 8 | ADS87894 | Ads87894 | Human pro |
| 23 | 2789 | 100.0 | 524 | 8 | ADU48630 | Adu48630 | Human pro |
| 24 | 2789 | 100.0 | 524 | 9 | ADW80727 | Adw80727 | Human pro |
| 25 | 2789 | 100.0 | 524 | 9 | ADX06774 | Adx06774 | Cyclin-de |
| 26 | 2789 | 100.0 | 524 | 9 | ADY14302 | Ady14302 | PRO polyp |
| 27 | 2789 | 100.0 | 524 | 9 | AED74803 | Aed74803 | Human pla |
| 28 | 2779 | 99.6 | 524 | 6 | ABU05208 | Abu05208 | Human exp |
| 29 | 2777.5 | 99.6 | 527 | 4 | AAB31915 | Aab31915 | Amino aci |
| 30 | 2777.5 | 99.6 | 527 | 5 | ABP68602 | Abp68602 | Human pan |
| 31 | 2777.5 | 99.6 | 527 | 6 | ABU79100 | Abu79100 | Lip-TAA b |
| 32 | 2777.5 | 99.6 | 527 | 6 | ABU05204 | Abu05204 | Human exp |
| 33 | 2777.5 | 99.6 | 527 | 6 | ABU05210 | Abu05210 | Human exp |
| 34 | 2777.5 | 99.6 | 527 | 7 | ADF43341 | Adf43341 | Superanti |
| 35 | 2772.5 | 99.4 | 523 | 4 | AAB31916 | Aab31916 | Amino aci |
| 36 | 2772.5 | 99.4 | 523 | 6 | ABU05211 | Abu05211 | Human exp |
| 37 | 2768 | 99.2 | 526 | 6 | ABU05209 | Abu05209 | Human exp |
| 38 | 2767.5 | 99.2 | 527 | 6 | ABU05206 | Abu05206 | Human exp |
| 39 | 2731 | 97.9 | 522 | 8 | ADU24090 | Adu24090 | Human cys |
| 40 | 2449.5 | 87.8 | 479 | 6 | ABR39442 | Abr39442 | Human GEN |
| 41 | 2024.5 | 72.6 | 385 | 6 | ABR41750 | Abr41750 | Human DIT |
| 42 | 1969 | 70.6 | 554 | 7 | ADB85295 | Adb85295 | Rat tubul |
| 43 | 1921 | 68.9 | 554 | 5 | ABB57102 | Abb57102 | Mouse isc |
| 44 | 1293.5 | 46.4 | 268 | 8 | ADP29875 | Adp29875 | Human sec |
| 45 | 1201 | 43.1 | 507 | 8 | ADS87898 | Ads87898 | Human hyp |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:21:31 ; Search time 65.0662 Seconds
(without alignments)
704.913 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|--------|---------|--------------|-------|--------------------------------------|
| 1 | 2789 | 100.0 | 524 | 2 | US-09-352-548-1 Sequence 1, Appli |
| 2 | 2789 | 100.0 | 524 | 2 | US-09-949-016-6272 Sequence 6272, Ap |
| 3 | 2789 | 100.0 | 524 | 2 | US-08-928-074-23 Sequence 23, Appl |
| 4 | 2789 | 100.0 | 535 | 2 | US-09-949-016-8603 Sequence 8603, Ap |
| 5 | 2766.5 | 99.2 | 523 | 1 | US-08-100-247-2 Sequence 2, Appli |
| 6 | 2766.5 | 99.2 | 523 | 2 | US-08-756-031-2 Sequence 2, Appli |
| 7 | 2759.5 | 98.9 | 523 | 1 | US-08-232-513A-3 Sequence 3, Appli |
| 8 | 2757.5 | 98.9 | 523 | 1 | US-08-483-146A-2 Sequence 2, Appli |
| 9 | 2757.5 | 98.9 | 523 | 1 | US-08-484-594A-2 Sequence 2, Appli |
| 10 | 2757.5 | 98.9 | 523 | 2 | US-09-076-258A-2 Sequence 2, Appli |
| 11 | 431 | 15.5 | 81 | 2 | US-09-352-548-2 Sequence 2, Appli |
| 12 | 418.5 | 15.0 | 80 | 1 | US-08-584-671-15 Sequence 15, Appl |
| 13 | 418.5 | 15.0 | 80 | 2 | US-09-027-376-15 Sequence 15, Appl |
| 14 | 418.5 | 15.0 | 80 | 6 | US-09-878-099-15 Sequence 15, Appl |
| 15 | 415.5 | 14.9 | 80 | 2 | US-09-094-192-15 Sequence 15, Appl |
| 16 | 412 | 14.8 | 80 | 1 | US-08-100-247-3 Sequence 3, Appli |
| 17 | 412 | 14.8 | 80 | 1 | US-08-483-146A-3 Sequence 3, Appli |
| 18 | 412 | 14.8 | 80 | 1 | US-08-232-513A-4 Sequence 4, Appli |
| 19 | 412 | 14.8 | 80 | 1 | US-08-484-594A-3 Sequence 3, Appli |

| | | | | | | |
|----|-------|------|-----|---|---------------------|-------------------|
| 20 | 412 | 14.8 | 80 | 2 | US-09-076-258A-3 | Sequence 3, Appli |
| 21 | 412 | 14.8 | 80 | 2 | US-08-756-031-3 | Sequence 3, Appli |
| 22 | 412 | 14.8 | 80 | 2 | US-08-928-074-24 | Sequence 24, Appl |
| 23 | 350.5 | 12.6 | 381 | 1 | US-09-193-877-2 | Sequence 2, Appli |
| 24 | 349.5 | 12.5 | 381 | 2 | US-09-949-016-10057 | Sequence 10057, A |
| 25 | 327 | 11.7 | 61 | 1 | US-08-584-671-13 | Sequence 13, Appl |
| 26 | 327 | 11.7 | 61 | 2 | US-09-027-376-13 | Sequence 13, Appl |
| 27 | 327 | 11.7 | 61 | 2 | US-09-094-192-13 | Sequence 13, Appl |
| 28 | 327 | 11.7 | 61 | 6 | US-09-878-099-13 | Sequence 13, Appl |
| 29 | 327 | 11.7 | 69 | 2 | US-09-268-070-2 | Sequence 2, Appli |
| 30 | 322 | 11.5 | 79 | 1 | US-08-584-671-16 | Sequence 16, Appl |
| 31 | 322 | 11.5 | 79 | 2 | US-09-027-376-16 | Sequence 16, Appl |
| 32 | 322 | 11.5 | 79 | 2 | US-09-094-192-16 | Sequence 16, Appl |
| 33 | 322 | 11.5 | 79 | 6 | US-09-878-099-16 | Sequence 16, Appl |
| 34 | 321 | 11.5 | 79 | 1 | US-08-584-671-14 | Sequence 14, Appl |
| 35 | 321 | 11.5 | 79 | 2 | US-09-027-376-14 | Sequence 14, Appl |
| 36 | 321 | 11.5 | 79 | 2 | US-09-094-192-14 | Sequence 14, Appl |
| 37 | 321 | 11.5 | 79 | 6 | US-09-878-099-14 | Sequence 14, Appl |
| 38 | 268.5 | 9.6 | 257 | 2 | US-08-596-684F-7 | Sequence 7, Appli |
| 39 | 239.5 | 8.6 | 60 | 1 | US-08-584-671-12 | Sequence 12, Appl |
| 40 | 239.5 | 8.6 | 60 | 2 | US-09-027-376-12 | Sequence 12, Appl |
| 41 | 239.5 | 8.6 | 60 | 2 | US-09-268-070-4 | Sequence 4, Appli |
| 42 | 239.5 | 8.6 | 60 | 2 | US-09-094-192-12 | Sequence 12, Appl |
| 43 | 239.5 | 8.6 | 60 | 6 | US-09-878-099-12 | Sequence 12, Appl |
| 44 | 238.5 | 8.6 | 68 | 2 | US-09-268-070-1 | Sequence 1, Appli |
| 45 | 211 | 7.6 | 40 | 2 | US-09-780-438C-1 | Sequence 1, Appli |
| 46 | 208 | 7.5 | 67 | 2 | US-09-268-070-3 | Sequence 3, Appli |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:23:10 ; Search time 216.887 Seconds
(without alignments)
1119.127 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|---------------------|-------------------|
| 1 | 2789 | 100.0 | 524 | 3 | US-09-870-759-60 | Sequence 60, Appl |
| 2 | 2789 | 100.0 | 524 | 3 | US-09-751-708A-60 | Sequence 60, Appl |
| 3 | 2789 | 100.0 | 524 | 4 | US-10-267-502-386 | Sequence 386, App |
| 4 | 2789 | 100.0 | 524 | 4 | US-10-408-765A-1207 | Sequence 1207, Ap |
| 5 | 2789 | 100.0 | 524 | 4 | US-10-746-442-23 | Sequence 23, Appl |
| 6 | 2789 | 100.0 | 524 | 4 | US-10-428-817A-56 | Sequence 56, Appl |
| 7 | 2789 | 100.0 | 524 | 5 | US-10-801-517-1 | Sequence 1, Appli |
| 8 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1865 | Sequence 1865, Ap |
| 9 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1866 | Sequence 1866, Ap |
| 10 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1868 | Sequence 1868, Ap |
| 11 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1869 | Sequence 1869, Ap |
| 12 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1871 | Sequence 1871, Ap |
| 13 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1873 | Sequence 1873, Ap |
| 14 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1878 | Sequence 1878, Ap |
| 15 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1879 | Sequence 1879, Ap |
| 16 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1880 | Sequence 1880, Ap |
| 17 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1881 | Sequence 1881, Ap |
| 18 | 2789 | 100.0 | 524 | 5 | US-10-473-127-1882 | Sequence 1882, Ap |
| 19 | 2789 | 100.0 | 524 | 5 | US-10-473-127-2041 | Sequence 2041, Ap |
| 20 | 2789 | 100.0 | 524 | 5 | US-10-821-234-1631 | Sequence 1631, Ap |

| | | | | | | |
|----|--------|-------|-----|---|--------------------|-------------------|
| 21 | 2789 | 100.0 | 524 | 6 | US-11-036-867-23 | Sequence 23, Appl |
| 22 | 2779 | 99.6 | 524 | 5 | US-10-473-127-1874 | Sequence 1874, Ap |
| 23 | 2777.5 | 99.6 | 527 | 3 | US-09-870-759-61 | Sequence 61, Appl |
| 24 | 2777.5 | 99.6 | 527 | 3 | US-09-751-708A-61 | Sequence 61, Appl |
| 25 | 2777.5 | 99.6 | 527 | 4 | US-10-060-036-73 | Sequence 73, Appl |
| 26 | 2777.5 | 99.6 | 527 | 4 | US-10-428-817A-57 | Sequence 57, Appl |
| 27 | 2777.5 | 99.6 | 527 | 5 | US-10-473-127-1870 | Sequence 1870, Ap |
| 28 | 2777.5 | 99.6 | 527 | 5 | US-10-473-127-1876 | Sequence 1876, Ap |
| 29 | 2772.5 | 99.4 | 523 | 5 | US-10-473-127-1877 | Sequence 1877, Ap |
| 30 | 2768 | 99.2 | 526 | 5 | US-10-473-127-1875 | Sequence 1875, Ap |
| 31 | 2767.5 | 99.2 | 527 | 5 | US-10-473-127-1872 | Sequence 1872, Ap |
| 32 | 2757.5 | 98.9 | 523 | 3 | US-09-767-007A-2 | Sequence 2, Appli |
| 33 | 2731 | 97.9 | 522 | 5 | US-10-618-281-38 | Sequence 38, Appl |
| 34 | 2449.5 | 87.8 | 479 | 3 | US-09-978-418-40 | Sequence 40, Appl |
| 35 | 2449.5 | 87.8 | 479 | 5 | US-10-485-231-40 | Sequence 40, Appl |
| 36 | 1969 | 70.6 | 554 | 4 | US-10-205-194-176 | Sequence 176, App |
| 37 | 1201 | 43.1 | 521 | 4 | US-10-276-162-1 | Sequence 1, Appli |
| 38 | 1201 | 43.1 | 521 | 6 | US-11-002-844-1 | Sequence 1, Appli |
| 39 | 1151.5 | 41.3 | 227 | 4 | US-10-452-858C-11 | Sequence 11, Appl |
| 40 | 1139.5 | 40.9 | 531 | 3 | US-09-833-245-903 | Sequence 903, App |
| 41 | 1139.5 | 40.9 | 531 | 6 | US-11-264-096-903 | Sequence 903, App |
| 42 | 1125 | 40.3 | 210 | 5 | US-10-473-127-1867 | Sequence 1867, Ap |
| 43 | 1093 | 39.2 | 209 | 4 | US-10-043-487-340 | Sequence 340, App |
| 44 | 834.5 | 29.9 | 362 | 4 | US-10-332-426-8 | Sequence 8, Appli |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:24:17 ; Search time 43.3775 Seconds
(without alignments)
959.216 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|--------|---------|--------------|-------|--|
| 1 | 2777.5 | 99.6 | 527 | 7 | US-11-450-360-27 Sequence 27, Appl |
| 2 | 2772.5 | 99.4 | 523 | 7 | US-11-450-360-28 Sequence 28, Appl |
| 3 | 545 | 19.5 | 241 | 7 | US-11-293-697-4529 Sequence 4529, Ap |
| 4 | 426.5 | 15.3 | 85 | 7 | US-11-450-360-24 Sequence 24, Appl |
| 5 | 414.5 | 14.9 | 83 | 7 | US-11-450-360-74 Sequence 74, Appl |
| 6 | 350.5 | 12.6 | 381 | 7 | US-11-450-360-25 Sequence 25, Appl |
| 7 | 335 | 12.0 | 380 | 7 | US-11-450-360-29 Sequence 29, Appl |
| 8 | 322.5 | 11.6 | 379 | 7 | US-11-450-360-26 Sequence 26, Appl |
| 9 | 292.5 | 10.5 | 370 | 6 | US-10-527-191-111 Sequence 111, App |
| 10 | 213 | 7.6 | 213 | 7 | US-11-056-355B-38055 Sequence 38055, A |
| 11 | 212 | 7.6 | 213 | 7 | US-11-056-355B-38404 Sequence 38404, A |
| 12 | 212 | 7.6 | 224 | 7 | US-11-056-355B-38403 Sequence 38403, A |
| 13 | 203.5 | 7.3 | 217 | 6 | US-10-953-349-1507 Sequence 1507, Ap |
| 14 | 203.5 | 7.3 | 217 | 7 | US-11-056-355B-35428 Sequence 35428, A |
| 15 | 203.5 | 7.3 | 217 | 7 | US-11-056-355B-77551 Sequence 77551, A |
| 16 | 186.5 | 6.7 | 217 | 7 | US-11-056-355B-5699 Sequence 5699, Ap |
| 17 | 186.5 | 6.7 | 224 | 7 | US-11-056-355B-5698 Sequence 5698, Ap |
| 18 | 184.5 | 6.6 | 184 | 7 | US-11-056-355B-5700 Sequence 5700, Ap |

| | | | | | | |
|----|-------|-----|-----|---|-----------------------|-------------------|
| 19 | 184.5 | 6.6 | 223 | 6 | US-10-449-902-38871 | Sequence 38871, A |
| 20 | 178.5 | 6.4 | 226 | 6 | US-10-449-902-45769 | Sequence 45769, A |
| 21 | 176.5 | 6.3 | 205 | 7 | US-11-056-355B-51890 | Sequence 51890, A |
| 22 | 176.5 | 6.3 | 233 | 7 | US-11-056-355B-51889 | Sequence 51889, A |
| 23 | 176.5 | 6.3 | 235 | 7 | US-11-056-355B-51888 | Sequence 51888, A |
| 24 | 175.5 | 6.3 | 229 | 7 | US-11-056-355B-12182 | Sequence 12182, A |
| 25 | 171.5 | 6.1 | 205 | 6 | US-10-953-349-7666 | Sequence 7666, Ap |
| 26 | 171.5 | 6.1 | 205 | 7 | US-11-056-355B-30348 | Sequence 30348, A |
| 27 | 171.5 | 6.1 | 205 | 7 | US-11-056-355B-33938 | Sequence 33938, A |
| 28 | 171.5 | 6.1 | 205 | 7 | US-11-056-355B-65080 | Sequence 65080, A |
| 29 | 171.5 | 6.1 | 233 | 7 | US-11-056-355B-65079 | Sequence 65079, A |
| 30 | 171.5 | 6.1 | 235 | 7 | US-11-056-355B-65078 | Sequence 65078, A |
| 31 | 171.5 | 6.1 | 242 | 6 | US-10-953-349-7665 | Sequence 7665, Ap |
| 32 | 171.5 | 6.1 | 242 | 7 | US-11-056-355B-30347 | Sequence 30347, A |
| 33 | 171.5 | 6.1 | 242 | 7 | US-11-056-355B-33937 | Sequence 33937, A |
| 34 | 171.5 | 6.1 | 278 | 6 | US-10-953-349-7664 | Sequence 7664, Ap |
| 35 | 171.5 | 6.1 | 278 | 7 | US-11-056-355B-30346 | Sequence 30346, A |
| 36 | 171.5 | 6.1 | 278 | 7 | US-11-056-355B-33936 | Sequence 33936, A |
| 37 | 171.5 | 6.1 | 298 | 7 | US-11-056-355B-28197 | Sequence 28197, A |
| 38 | 171.5 | 6.1 | 298 | 7 | US-11-056-355B-31787 | Sequence 31787, A |
| 39 | 171.5 | 6.1 | 298 | 7 | US-11-056-355B-47637 | Sequence 47637, A |
| 40 | 171.5 | 6.1 | 298 | 7 | US-11-056-355B-97531 | Sequence 97531, A |
| 41 | 171.5 | 6.1 | 298 | 7 | US-11-056-355B-108770 | Sequence 108770, |
| 42 | 171.5 | 6.1 | 486 | 7 | US-11-056-355B-97530 | Sequence 97530, A |
| 43 | 171.5 | 6.1 | 486 | 7 | US-11-056-355B-108769 | Sequence 108769, |
| 44 | 171.5 | 6.1 | 506 | 7 | US-11-056-355B-28196 | Sequence 28196, A |
| 45 | 171.5 | 6.1 | 506 | 7 | US-11-056-355B-31786 | Sequence 31786, A |

GenCore version 5.1.9

Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:17:40 ; Search time 45.1126 Seconds
 (without alignments)
 1117.595 Million cell updates/sec

Title: US-10-801-517-1
 Perfect score: 2789
 Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|--------|---------|--------------|----------|--------------------|
| 1 | 2777.5 | 99.6 | 527 | 1 SAHUP | saposin precursor |
| 2 | 1996 | 71.6 | 554 | 1 A28716 | saposin precursor |
| 3 | 1937.5 | 69.5 | 557 | 1 JH0604 | saposin precursor |
| 4 | 511 | 18.3 | 965 | 2 T00207 | P109 protein - sil |
| 5 | 389 | 13.9 | 79 | 2 A49475 | cerebroside sulfat |
| 6 | 379 | 13.6 | 376 | 2 S02766 | pulmonary surfacta |
| 7 | 348.5 | 12.5 | 381 | 1 LNHUB | pulmonary surfacta |
| 8 | 343 | 12.3 | 80 | 2 S21770 | saposin-C - bovine |
| 9 | 310 | 11.1 | 363 | 2 A29072 | pulmonary surfacta |
| 10 | 301.5 | 10.8 | 369 | 2 I46531 | surfactant protein |
| 11 | 261 | 9.4 | 81 | 2 A32026 | glucosylceramide b |
| 12 | 256.5 | 9.2 | 370 | 1 LNRBB | pulmonary surfacta |
| 13 | 213 | 7.6 | 213 | 2 T46069 | hypothetical prote |
| 14 | 203.5 | 7.3 | 217 | 2 T48201 | hypothetical prote |
| 15 | 176.5 | 6.3 | 402 | 2 T15677 | hypothetical prote |
| 16 | 173.5 | 6.2 | 513 | 2 T09739 | aspartic endopepti |
| 17 | 171.5 | 6.1 | 506 | 2 F86253 | hypothetical prote |
| 18 | 165.5 | 5.9 | 506 | 2 T07915 | probable aspartic |
| 19 | 161.5 | 5.8 | 513 | 2 T11686 | aspartic proteinas |
| 20 | 161 | 5.8 | 428 | 2 S47096 | cynarase (EC 3.4.2 |
| 21 | 161 | 5.8 | 474 | 2 T12049 | cyprosin (EC 3.4.2 |
| 22 | 158.5 | 5.7 | 508 | 2 S19697 | aspartic proteinas |

| | | | | | | |
|----|-------|-----|------|---|--------|--------------------|
| 23 | 156 | 5.6 | 314 | 2 | T15674 | hypothetical prote |
| 24 | 155.5 | 5.6 | 292 | 2 | T14446 | aspartic proteinas |
| 25 | 155.5 | 5.6 | 322 | 2 | S41400 | aspartic proteinas |
| 26 | 154 | 5.5 | 496 | 2 | JS0732 | aspartic proteinas |
| 27 | 153.5 | 5.5 | 509 | 2 | JC7272 | aspartic proteinas |
| 28 | 145.5 | 5.2 | 205 | 2 | B89567 | protein T08A9.7 [i |
| 29 | 143.5 | 5.1 | 1175 | 2 | S52417 | E-selectin ligand- |
| 30 | 142.5 | 5.1 | 509 | 2 | S49349 | cyprosin (EC 3.4.2 |
| 31 | 142.5 | 5.1 | 509 | 2 | S66516 | oryzasin (EC 3.4.2 |
| 32 | 142.5 | 5.1 | 1948 | 2 | S00485 | gene 11-1 protein |
| 33 | 141 | 5.1 | 508 | 2 | D85056 | probable aspartic |
| 34 | 134 | 4.8 | 1927 | 2 | G64585 | cag pathogenicity |
| 35 | 132.5 | 4.8 | 433 | 2 | E96649 | hypothetical prote |
| 36 | 127.5 | 4.6 | 280 | 2 | PC4080 | aspartic proteinas |
| 37 | 127.5 | 4.6 | 1142 | 2 | A45031 | cysteine-rich fibr |
| 38 | 126.5 | 4.5 | 195 | 2 | T15676 | hypothetical prote |
| 39 | 126.5 | 4.5 | 1819 | 2 | A71928 | cag island protein |
| 40 | 126 | 4.5 | 506 | 2 | S71591 | aspartic proteinas |
| 41 | 123.5 | 4.4 | 370 | 2 | E96502 | hypothetical prote |
| 42 | 119 | 4.3 | 661 | 2 | S67177 | hypothetical prote |
| 43 | 116.5 | 4.2 | 652 | 2 | F85017 | probable CHP-rich |
| 44 | 116.5 | 4.2 | 707 | 2 | T26218 | hypothetical prote |
| 45 | 116 | 4.2 | 975 | 2 | I59422 | rsec8 - rat (fragm |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:17:37 ; Search time 153.556 Seconds
(without alignments)
3156.550 Million cell updates/sec

Title: US-10-801-517-1
Perfect score: 2789
Sequence: 1 MYALFLLASLLGAALAGPVL.....NTETAAQCNAVEHCKRHVWN 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|--------|---------|--------------|-------|---------------------------------|
| 1 | 2789 | 100.0 | 524 | 1 | SAP_HUMAN P07602 h proactiva |
| 2 | 2789 | 100.0 | 524 | 2 | Q5JQ36_HUMAN Q5jq36 homo sapien |
| 3 | 2785 | 99.9 | 524 | 2 | Q53FJ5_HUMAN Q53fj5 homo sapien |
| 4 | 2783 | 99.8 | 559 | 2 | Q5JQ37_HUMAN Q5jq37 homo sapien |
| 5 | 2777.5 | 99.6 | 530 | 2 | Q59EN5_HUMAN Q59en5 homo sapien |
| 6 | 2776.5 | 99.6 | 527 | 2 | Q5NVD5_PONPY Q5nvd5 pongo pygma |
| 7 | 2770 | 99.3 | 526 | 2 | Q5R4U7_PONPY Q5r4u7 pongo pygma |
| 8 | 2451.5 | 87.9 | 497 | 2 | Q4R590_MACFA Q4r590 m brain cdn |
| 9 | 2425.5 | 87.0 | 525 | 1 | SAP_BOVIN P26779 b proactiva |
| 10 | 2374.5 | 85.1 | 452 | 2 | Q5R406_PONPY Q5r406 pongo pygma |
| 11 | 1996 | 71.6 | 554 | 1 | SAP_RAT P10960 rattus norv |
| 12 | 1982.5 | 71.1 | 553 | 2 | Q6P7A4_RAT Q6p7a4 rattus norv |
| 13 | 1955 | 70.1 | 554 | 2 | Q3TKB2_MOUSE Q3tkb2 mus musculu |
| 14 | 1953 | 70.0 | 554 | 2 | Q3U897_MOUSE Q3u897 mus musculu |
| 15 | 1952 | 70.0 | 554 | 2 | Q3TKK3_MOUSE Q3tkk3 mus musculu |
| 16 | 1950 | 69.9 | 554 | 2 | Q8BFQ1_MOUSE Q8bfq1 m 2 days ne |
| 17 | 1948 | 69.8 | 554 | 2 | Q3TWE9_MOUSE Q3twe9 mus musculu |
| 18 | 1947 | 69.8 | 554 | 2 | Q3TID4_MOUSE Q3tid4 mus musculu |
| 19 | 1947 | 69.8 | 554 | 2 | Q3TWL8_MOUSE Q3twl8 mus musculu |
| 20 | 1946 | 69.8 | 554 | 2 | Q3U825_MOUSE Q3u825 mus musculu |
| 21 | 1946 | 69.8 | 554 | 2 | Q3U8C4_MOUSE Q3u8c4 mus musculu |
| 22 | 1945 | 69.7 | 554 | 2 | Q3TIT5_MOUSE Q3tit5 mus musculu |
| 23 | 1944 | 69.7 | 554 | 2 | Q3U5W2_MOUSE Q3u5w2 mus musculu |
| 24 | 1941 | 69.6 | 554 | 2 | Q3TWF9_MOUSE Q3twf9 mus musculu |

| | | | | | | | | |
|----|--------|------|-----|---|--------------|--------|-------------|-----------|
| 25 | 1940 | 69.6 | 554 | 2 | Q3TXP9_MOUSE | Q3txp9 | mus | musculu |
| 26 | 1938.5 | 69.5 | 553 | 2 | Q3TXJ0_MOUSE | Q3txj0 | m | osteoclas |
| 27 | 1938.5 | 69.5 | 557 | 1 | SAP_MOUSE | Q61207 | mus | musculu |
| 28 | 1938.5 | 69.5 | 557 | 2 | Q3UFE8_MOUSE | Q3ufe8 | mus | musculu |
| 29 | 1900 | 68.1 | 551 | 2 | Q3UE29_MOUSE | Q3ue29 | mus | musculu |
| 30 | 1899.5 | 68.1 | 545 | 2 | Q3UAS4_MOUSE | Q3uas4 | m | bone marr |
| 31 | 1887 | 67.7 | 527 | 2 | Q3TWM9_MOUSE | Q3twm9 | mus | musculu |
| 32 | 1679.5 | 60.2 | 518 | 1 | SAP_CHICK | Q13035 | gallus | gall |
| 33 | 1442 | 51.7 | 512 | 2 | Q7SY70_XENLA | Q7sy70 | xenopus | lae |
| 34 | 1429 | 51.2 | 518 | 2 | Q642S6_XENLA | Q642s6 | xenopus | lae |
| 35 | 1416 | 50.8 | 550 | 2 | Q4RQ38_TETNG | Q4rq38 | tetraodon | n |
| 36 | 1414 | 50.7 | 520 | 2 | Q8UVZ4_BRARE | Q8uvz4 | brachydanio | |
| 37 | 1412 | 50.6 | 520 | 2 | Q6PH48_BRARE | Q6ph48 | brachydanio | |
| 38 | 1411 | 50.6 | 520 | 2 | Q6P3G7_BRARE | Q6p3g7 | brachydanio | |
| 39 | 1343 | 48.2 | 522 | 2 | Q9DG82_BRARE | Q9dg82 | brachydanio | |
| 40 | 1201 | 43.1 | 543 | 2 | Q6NUJ1_HUMAN | Q6nuj1 | homo | sapien |
| 41 | 1153 | 41.3 | 240 | 2 | Q5BJH1_HUMAN | Q5bjh1 | homo | sapien |
| 42 | 1099.5 | 39.4 | 525 | 2 | Q8C1C1_MOUSE | Q8c1c1 | mus | musculu |
| 43 | 803 | 28.8 | 245 | 2 | Q5ZL62_CHICK | Q5zl62 | gallus | gall |
| 44 | 786 | 28.2 | 449 | 2 | Q8BJV5_MOUSE | Q8bjv5 | mus | musculu |
| 45 | 772 | 27.7 | 402 | 2 | Q8C1N0_MOUSE | Q8c1n0 | mus | musculu |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:13:58 ; Search time 15.4967 Seconds
(without alignments)
2360.331 Million cell updates/sec

Title: US-10-801-517-2
Perfect score: 412
Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPELVCSMLHLCSG_80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------|--------------------|
| 1 | 412 | 100.0 | 80 | 2 | AAR70784 | Aar70784 Saposin-C |
| 2 | 412 | 100.0 | 80 | 2 | AAW85653 | Aaw85653 Human sap |
| 3 | 412 | 100.0 | 80 | 4 | AAU05697 | Aau05697 Human Sap |
| 4 | 412 | 100.0 | 80 | 7 | ABU62252 | Abu62252 Sphingoli |
| 5 | 412 | 100.0 | 80 | 8 | ADQ94329 | Adq94329 Human Pre |
| 6 | 412 | 100.0 | 80 | 8 | ADU48631 | Adu48631 Human Sap |
| 7 | 412 | 100.0 | 80 | 9 | ADW80728 | Adw80728 Human sap |
| 8 | 412 | 100.0 | 80 | 9 | ADZ88479 | Adz88479 Human sap |
| 9 | 412 | 100.0 | 210 | 6 | ABU05201 | Abu05201 Human exp |
| 10 | 412 | 100.0 | 385 | 6 | ABR41750 | Abr41750 Human DIT |
| 11 | 412 | 100.0 | 479 | 6 | ABR39442 | Abr39442 Human GEN |
| 12 | 412 | 100.0 | 522 | 8 | ADU24090 | Adu24090 Human cys |
| 13 | 412 | 100.0 | 523 | 4 | AAB31916 | Aab31916 Amino aci |
| 14 | 412 | 100.0 | 523 | 6 | ABU05211 | Abu05211 Human exp |
| 15 | 412 | 100.0 | 524 | 2 | AAR70783 | Aar70783 Prosaposi |
| 16 | 412 | 100.0 | 524 | 2 | AAW85652 | Aaw85652 Human pro |

| | | | | | | | |
|----|-------|-------|-----|---|----------|----------|-----------|
| 17 | 412 | 100.0 | 524 | 3 | AAy58716 | Aay58716 | Human pro |
| 18 | 412 | 100.0 | 524 | 6 | ABU79099 | Abu79099 | Lip-TAA b |
| 19 | 412 | 100.0 | 524 | 6 | ABU05200 | Abu05200 | Human exp |
| 20 | 412 | 100.0 | 524 | 6 | ABU05207 | Abu05207 | Human exp |
| 21 | 412 | 100.0 | 524 | 6 | ABU05203 | Abu05203 | Human exp |
| 22 | 412 | 100.0 | 524 | 6 | ABU07340 | Abu07340 | Human exp |
| 23 | 412 | 100.0 | 524 | 6 | ABU05216 | Abu05216 | Human exp |
| 24 | 412 | 100.0 | 524 | 6 | ABU05202 | Abu05202 | Human exp |
| 25 | 412 | 100.0 | 524 | 6 | ABU05208 | Abu05208 | Human exp |
| 26 | 412 | 100.0 | 524 | 6 | ABU05214 | Abu05214 | Human exp |
| 27 | 412 | 100.0 | 524 | 6 | ABU05215 | Abu05215 | Human exp |
| 28 | 412 | 100.0 | 524 | 6 | ABU05199 | Abu05199 | Human exp |
| 29 | 412 | 100.0 | 524 | 6 | ABU05212 | Abu05212 | Human exp |
| 30 | 412 | 100.0 | 524 | 6 | ABU05213 | Abu05213 | Human exp |
| 31 | 412 | 100.0 | 524 | 6 | ABU05205 | Abu05205 | Human exp |
| 32 | 412 | 100.0 | 524 | 7 | ADF43340 | Adf43340 | Superanti |
| 33 | 412 | 100.0 | 524 | 7 | ADJ69401 | Adj69401 | Human hea |
| 34 | 412 | 100.0 | 524 | 8 | ADO08060 | Ado08060 | Human pol |
| 35 | 412 | 100.0 | 524 | 8 | ADQ94328 | Adq94328 | Human Pre |
| 36 | 412 | 100.0 | 524 | 8 | ABM81149 | Abm81149 | Tumour-as |
| 37 | 412 | 100.0 | 524 | 8 | ADS87894 | Ads87894 | Human pro |
| 38 | 412 | 100.0 | 524 | 8 | ADU48630 | Adu48630 | Human pro |
| 39 | 412 | 100.0 | 524 | 9 | ADW80727 | Adw80727 | Human pro |
| 40 | 412 | 100.0 | 524 | 9 | ADX06774 | Adx06774 | Cyclin-de |
| 41 | 412 | 100.0 | 524 | 9 | ADY14302 | Ady14302 | PRO polyp |
| 42 | 412 | 100.0 | 524 | 9 | AED74803 | Aed74803 | Human pla |
| 43 | 412 | 100.0 | 526 | 6 | ABU05209 | Abu05209 | Human exp |
| 44 | 412 | 100.0 | 527 | 4 | AAB31915 | Aab31915 | Amino aci |
| 45 | 412 | 100.0 | 527 | 5 | ABP68602 | Abp68602 | Human pan |
| 46 | 412 | 100.0 | 527 | 6 | ABU79100 | Abu79100 | Lip-TAA b |
| 47 | 412 | 100.0 | 527 | 6 | ABU05206 | Abu05206 | Human exp |
| 48 | 412 | 100.0 | 527 | 6 | ABU05204 | Abu05204 | Human exp |
| 49 | 412 | 100.0 | 527 | 6 | ABU05210 | Abu05210 | Human exp |
| 50 | 412 | 100.0 | 527 | 7 | ADF43341 | Adf43341 | Superanti |
| 51 | 412 | 100.0 | 592 | 4 | AAU05698 | Aau05698 | Human glu |
| 52 | 355 | 86.2 | 227 | 8 | ADO57419 | Ado57419 | Hairless |
| 53 | 283.5 | 68.8 | 268 | 8 | ADP29875 | Adp29875 | Human sec |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:21:31 ; Search time 9.93377 Seconds
(without alignments)
704.913 Million cell updates/sec

Title: US-10-801-517-2
Perfect score: 412
Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPELVCSMLHLCSG 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|--------------------|-------------------|
| 1 | 412 | 100.0 | 80 | 1 | US-08-100-247-3 | Sequence 3, Appli |
| 2 | 412 | 100.0 | 80 | 1 | US-08-483-146A-3 | Sequence 3, Appli |
| 3 | 412 | 100.0 | 80 | 1 | US-08-232-513A-4 | Sequence 4, Appli |
| 4 | 412 | 100.0 | 80 | 1 | US-08-484-594A-3 | Sequence 3, Appli |
| 5 | 412 | 100.0 | 80 | 2 | US-09-076-258A-3 | Sequence 3, Appli |
| 6 | 412 | 100.0 | 80 | 2 | US-08-756-031-3 | Sequence 3, Appli |
| 7 | 412 | 100.0 | 80 | 2 | US-08-928-074-24 | Sequence 24, Appl |
| 8 | 412 | 100.0 | 523 | 1 | US-08-100-247-2 | Sequence 2, Appli |
| 9 | 412 | 100.0 | 523 | 1 | US-08-483-146A-2 | Sequence 2, Appli |
| 10 | 412 | 100.0 | 523 | 1 | US-08-232-513A-3 | Sequence 3, Appli |
| 11 | 412 | 100.0 | 523 | 1 | US-08-484-594A-2 | Sequence 2, Appli |
| 12 | 412 | 100.0 | 523 | 2 | US-09-076-258A-2 | Sequence 2, Appli |
| 13 | 412 | 100.0 | 523 | 2 | US-08-756-031-2 | Sequence 2, Appli |
| 14 | 412 | 100.0 | 524 | 2 | US-09-352-548-1 | Sequence 1, Appli |
| 15 | 412 | 100.0 | 524 | 2 | US-09-949-016-6272 | Sequence 6272, Ap |
| 16 | 412 | 100.0 | 524 | 2 | US-08-928-074-23 | Sequence 23, Appl |
| 17 | 412 | 100.0 | 535 | 2 | US-09-949-016-8603 | Sequence 8603, Ap |
| 18 | 211 | 51.2 | 40 | 2 | US-09-780-438C-1 | Sequence 1, Appli |
| 19 | 201 | 48.8 | 38 | 2 | US-09-780-438C-2 | Sequence 2, Appli |

| | | | | | | |
|----|------|------|-----|---|---------------------|-------------------|
| 20 | 111 | 26.9 | 22 | 1 | US-08-100-247-1 | Sequence 1, Appli |
| 21 | 111 | 26.9 | 22 | 1 | US-08-483-146A-1 | Sequence 1, Appli |
| 22 | 111 | 26.9 | 22 | 1 | US-08-232-513A-1 | Sequence 1, Appli |
| 23 | 111 | 26.9 | 22 | 1 | US-08-484-594A-1 | Sequence 1, Appli |
| 24 | 111 | 26.9 | 22 | 2 | US-09-231-159-1 | Sequence 1, Appli |
| 25 | 111 | 26.9 | 22 | 2 | US-08-611-307-1 | Sequence 1, Appli |
| 26 | 111 | 26.9 | 22 | 2 | US-09-148-030-1 | Sequence 1, Appli |
| 27 | 111 | 26.9 | 22 | 2 | US-09-076-258A-1 | Sequence 1, Appli |
| 28 | 111 | 26.9 | 22 | 2 | US-08-756-031-1 | Sequence 1, Appli |
| 29 | 111 | 26.9 | 22 | 2 | US-08-928-074-1 | Sequence 1, Appli |
| 30 | 106 | 25.7 | 22 | 2 | US-09-231-159-8 | Sequence 8, Appli |
| 31 | 106 | 25.7 | 22 | 2 | US-08-611-307-8 | Sequence 8, Appli |
| 32 | 106 | 25.7 | 22 | 2 | US-08-928-074-8 | Sequence 8, Appli |
| 33 | 101 | 24.5 | 38 | 2 | US-09-780-438C-3 | Sequence 3, Appli |
| 34 | 101 | 24.5 | 38 | 2 | US-09-780-438C-5 | Sequence 5, Appli |
| 35 | 101 | 24.5 | 38 | 2 | US-09-780-438C-6 | Sequence 6, Appli |
| 36 | 101 | 24.5 | 39 | 2 | US-09-780-438C-4 | Sequence 4, Appli |
| 37 | 96 | 23.3 | 22 | 1 | US-08-483-146A-9 | Sequence 9, Appli |
| 38 | 96 | 23.3 | 22 | 1 | US-08-232-513A-18 | Sequence 18, Appl |
| 39 | 96 | 23.3 | 22 | 1 | US-08-484-594A-9 | Sequence 9, Appli |
| 40 | 96 | 23.3 | 22 | 2 | US-09-231-159-7 | Sequence 7, Appli |
| 41 | 96 | 23.3 | 22 | 2 | US-08-611-307-7 | Sequence 7, Appli |
| 42 | 96 | 23.3 | 22 | 2 | US-09-076-258A-9 | Sequence 9, Appli |
| 43 | 96 | 23.3 | 22 | 2 | US-08-928-074-7 | Sequence 7, Appli |
| 44 | 96 | 23.3 | 514 | 2 | US-10-339-351-2 | Sequence 2, Appli |
| 45 | 92 | 22.3 | 79 | 2 | US-08-596-684F-6 | Sequence 6, Appli |
| 46 | 92 | 22.3 | 79 | 2 | US-09-515-356-1 | Sequence 1, Appli |
| 47 | 92 | 22.3 | 181 | 2 | US-08-848-580-12 | Sequence 12, Appl |
| 48 | 92 | 22.3 | 181 | 2 | US-08-488-123-12 | Sequence 12, Appl |
| 49 | 92 | 22.3 | 257 | 2 | US-08-596-684F-7 | Sequence 7, Appli |
| 50 | 92 | 22.3 | 381 | 2 | US-09-949-016-10057 | Sequence 10057, A |
| 51 | 91 | 22.1 | 79 | 2 | US-09-788-308E-2 | Sequence 2, Appli |
| 52 | 91 | 22.1 | 381 | 1 | US-09-193-877-2 | Sequence 2, Appli |
| 53 | 88 | 21.4 | 514 | 2 | US-10-339-351-1 | Sequence 1, Appli |
| 54 | 88 | 21.4 | 514 | 2 | US-10-339-351-3 | Sequence 3, Appli |
| 55 | 83 | 20.1 | 18 | 1 | US-08-100-247-5 | Sequence 5, Appli |
| 56 | 83 | 20.1 | 18 | 1 | US-08-483-146A-5 | Sequence 5, Appli |
| 57 | 83 | 20.1 | 18 | 1 | US-08-232-513A-6 | Sequence 6, Appli |
| 58 | 83 | 20.1 | 18 | 1 | US-08-484-594A-5 | Sequence 5, Appli |
| 59 | 83 | 20.1 | 18 | 2 | US-09-231-159-20 | Sequence 20, Appl |
| 60 | 83 | 20.1 | 18 | 2 | US-08-611-307-20 | Sequence 20, Appl |
| 61 | 83 | 20.1 | 18 | 2 | US-09-148-030-2 | Sequence 2, Appli |
| 62 | 83 | 20.1 | 18 | 2 | US-09-076-258A-5 | Sequence 5, Appli |
| 63 | 83 | 20.1 | 18 | 2 | US-08-756-031-5 | Sequence 5, Appli |
| 64 | 83 | 20.1 | 18 | 2 | US-08-928-074-20 | Sequence 20, Appl |
| 65 | 80.5 | 19.5 | 78 | 1 | US-08-732-228-1 | Sequence 1, Appli |
| 66 | 75 | 18.2 | 15 | 2 | US-09-148-030-10 | Sequence 10, Appl |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:23:10 ; Search time 33.1126 Seconds
(without alignments)
1119.127 Million cell updates/sec

Title: US-10-801-517-2
Perfect score: 412
Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPELVCSMLHLCSG 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|---------------------|-------------------|
| 1 | 412 | 100.0 | 80 | 3 | US-09-767-007A-3 | Sequence 3, Appli |
| 2 | 412 | 100.0 | 80 | 3 | US-09-753-126-3 | Sequence 3, Appli |
| 3 | 412 | 100.0 | 80 | 4 | US-10-330-697-3 | Sequence 3, Appli |
| 4 | 412 | 100.0 | 80 | 4 | US-10-746-442-24 | Sequence 24, Appl |
| 5 | 412 | 100.0 | 80 | 5 | US-10-801-517-2 | Sequence 2, Appli |
| 6 | 412 | 100.0 | 80 | 6 | US-11-036-867-24 | Sequence 24, Appl |
| 7 | 412 | 100.0 | 210 | 5 | US-10-473-127-1867 | Sequence 1867, Ap |
| 8 | 412 | 100.0 | 479 | 3 | US-09-978-418-40 | Sequence 40, Appl |
| 9 | 412 | 100.0 | 479 | 5 | US-10-485-231-40 | Sequence 40, Appl |
| 10 | 412 | 100.0 | 522 | 5 | US-10-618-281-38 | Sequence 38, Appl |
| 11 | 412 | 100.0 | 523 | 3 | US-09-767-007A-2 | Sequence 2, Appli |
| 12 | 412 | 100.0 | 523 | 5 | US-10-473-127-1877 | Sequence 1877, Ap |
| 13 | 412 | 100.0 | 524 | 3 | US-09-870-759-60 | Sequence 60, Appl |
| 14 | 412 | 100.0 | 524 | 3 | US-09-751-708A-60 | Sequence 60, Appl |
| 15 | 412 | 100.0 | 524 | 4 | US-10-267-502-386 | Sequence 386, App |
| 16 | 412 | 100.0 | 524 | 4 | US-10-408-765A-1207 | Sequence 1207, Ap |
| 17 | 412 | 100.0 | 524 | 4 | US-10-746-442-23 | Sequence 23, Appl |
| 18 | 412 | 100.0 | 524 | 4 | US-10-428-817A-56 | Sequence 56, Appl |
| 19 | 412 | 100.0 | 524 | 5 | US-10-801-517-1 | Sequence 1, Appli |
| 20 | 412 | 100.0 | 524 | 5 | US-10-473-127-1865 | Sequence 1865, Ap |

| | | | | | | |
|----|-----|-------|-----|---|--------------------|-------------------|
| 21 | 412 | 100.0 | 524 | 5 | US-10-473-127-1866 | Sequence 1866, Ap |
| 22 | 412 | 100.0 | 524 | 5 | US-10-473-127-1868 | Sequence 1868, Ap |
| 23 | 412 | 100.0 | 524 | 5 | US-10-473-127-1869 | Sequence 1869, Ap |
| 24 | 412 | 100.0 | 524 | 5 | US-10-473-127-1871 | Sequence 1871, Ap |
| 25 | 412 | 100.0 | 524 | 5 | US-10-473-127-1873 | Sequence 1873, Ap |
| 26 | 412 | 100.0 | 524 | 5 | US-10-473-127-1874 | Sequence 1874, Ap |
| 27 | 412 | 100.0 | 524 | 5 | US-10-473-127-1878 | Sequence 1878, Ap |
| 28 | 412 | 100.0 | 524 | 5 | US-10-473-127-1879 | Sequence 1879, Ap |
| 29 | 412 | 100.0 | 524 | 5 | US-10-473-127-1880 | Sequence 1880, Ap |
| 30 | 412 | 100.0 | 524 | 5 | US-10-473-127-1881 | Sequence 1881, Ap |
| 31 | 412 | 100.0 | 524 | 5 | US-10-473-127-1882 | Sequence 1882, Ap |
| 32 | 412 | 100.0 | 524 | 5 | US-10-473-127-2041 | Sequence 2041, Ap |
| 33 | 412 | 100.0 | 524 | 5 | US-10-821-234-1631 | Sequence 1631, Ap |
| 34 | 412 | 100.0 | 524 | 6 | US-11-036-867-23 | Sequence 23, Appl |
| 35 | 412 | 100.0 | 526 | 5 | US-10-473-127-1875 | Sequence 1875, Ap |
| 36 | 412 | 100.0 | 527 | 3 | US-09-870-759-61 | Sequence 61, Appl |
| 37 | 412 | 100.0 | 527 | 3 | US-09-751-708A-61 | Sequence 61, Appl |
| 38 | 412 | 100.0 | 527 | 4 | US-10-060-036-73 | Sequence 73, Appl |
| 39 | 412 | 100.0 | 527 | 4 | US-10-428-817A-57 | Sequence 57, Appl |
| 40 | 412 | 100.0 | 527 | 5 | US-10-473-127-1870 | Sequence 1870, Ap |
| 41 | 412 | 100.0 | 527 | 5 | US-10-473-127-1872 | Sequence 1872, Ap |
| 42 | 412 | 100.0 | 527 | 5 | US-10-473-127-1876 | Sequence 1876, Ap |
| 43 | 412 | 100.0 | 592 | 3 | US-09-753-126-4 | Sequence 4, Appli |
| 44 | 412 | 100.0 | 592 | 4 | US-10-330-697-4 | Sequence 4, Appli |
| 45 | 355 | 86.2 | 227 | 4 | US-10-452-858C-11 | Sequence 11, Appl |
| 46 | 257 | 62.4 | 209 | 4 | US-10-043-487-340 | Sequence 340, App |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:24:17 ; Search time 6.62252 Seconds
(without alignments)
959.216 Million cell updates/sec

Title: US-10-801-517-2
Perfect score: 412
Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPELVCSMLHLCSG 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|----------------------|
| 1 | 412 | 100.0 | 523 | 7 | US-11-450-360-28 |
| 2 | 412 | 100.0 | 527 | 7 | US-11-450-360-27 |
| 3 | 147.5 | 35.8 | 241 | 7 | US-11-293-697-4529 |
| 4 | 115 | 27.9 | 223 | 6 | US-10-449-902-38871 |
| 5 | 106.5 | 25.8 | 135 | 6 | US-10-953-349-1508 |
| 6 | 106.5 | 25.8 | 135 | 7 | US-11-056-355B-35429 |
| 7 | 106.5 | 25.8 | 135 | 7 | US-11-056-355B-77552 |
| 8 | 106.5 | 25.8 | 217 | 6 | US-10-953-349-1507 |
| 9 | 106.5 | 25.8 | 217 | 7 | US-11-056-355B-35428 |
| 10 | 106.5 | 25.8 | 217 | 7 | US-11-056-355B-77551 |
| 11 | 106 | 25.7 | 213 | 7 | US-11-056-355B-38055 |
| 12 | 106 | 25.7 | 213 | 7 | US-11-056-355B-38404 |
| 13 | 106 | 25.7 | 224 | 6 | US-10-953-349-16163 |
| 14 | 106 | 25.7 | 224 | 7 | US-11-056-355B-38403 |
| 15 | 106 | 25.7 | 224 | 7 | US-11-056-355B-55976 |
| 16 | 104 | 25.2 | 184 | 7 | US-11-056-355B-5700 |
| 17 | 104 | 25.2 | 205 | 6 | US-10-953-349-7666 |
| 18 | 104 | 25.2 | 205 | 7 | US-11-056-355B-30348 |

| | | | | | | |
|----|------|------|-----|---|-----------------------|--------------------|
| 19 | 104 | 25.2 | 205 | 7 | US-11-056-355B-33938 | Sequence 33938, A |
| 20 | 104 | 25.2 | 217 | 7 | US-11-056-355B-5699 | Sequence 5699, Ap |
| 21 | 104 | 25.2 | 224 | 7 | US-11-174-307B-4380 | Sequence 4380, Ap |
| 22 | 104 | 25.2 | 224 | 7 | US-11-056-355B-5698 | Sequence 5698, Ap |
| 23 | 104 | 25.2 | 242 | 6 | US-10-953-349-7665 | Sequence 7665, Ap |
| 24 | 104 | 25.2 | 242 | 7 | US-11-056-355B-30347 | Sequence 30347, A |
| 25 | 104 | 25.2 | 242 | 7 | US-11-056-355B-33937 | Sequence 33937, A |
| 26 | 104 | 25.2 | 278 | 6 | US-10-953-349-7664 | Sequence 7664, Ap |
| 27 | 104 | 25.2 | 278 | 7 | US-11-056-355B-30346 | Sequence 30346, A |
| 28 | 104 | 25.2 | 278 | 7 | US-11-056-355B-33936 | Sequence 33936, A |
| 29 | 104 | 25.2 | 298 | 7 | US-11-056-355B-28197 | Sequence 28197, A |
| 30 | 104 | 25.2 | 298 | 7 | US-11-056-355B-31787 | Sequence 31787, A |
| 31 | 104 | 25.2 | 298 | 7 | US-11-056-355B-47637 | Sequence 47637, A |
| 32 | 104 | 25.2 | 298 | 7 | US-11-056-355B-97531 | Sequence 97531, A |
| 33 | 104 | 25.2 | 298 | 7 | US-11-056-355B-108770 | Sequence 108770, A |
| 34 | 104 | 25.2 | 486 | 7 | US-11-056-355B-97530 | Sequence 97530, A |
| 35 | 104 | 25.2 | 486 | 7 | US-11-056-355B-108769 | Sequence 108769, A |
| 36 | 104 | 25.2 | 506 | 7 | US-11-056-355B-28196 | Sequence 28196, A |
| 37 | 104 | 25.2 | 506 | 7 | US-11-056-355B-31786 | Sequence 31786, A |
| 38 | 104 | 25.2 | 506 | 7 | US-11-056-355B-47636 | Sequence 47636, A |
| 39 | 104 | 25.2 | 522 | 7 | US-11-056-355B-28195 | Sequence 28195, A |
| 40 | 104 | 25.2 | 522 | 7 | US-11-056-355B-31785 | Sequence 31785, A |
| 41 | 104 | 25.2 | 522 | 7 | US-11-056-355B-47635 | Sequence 47635, A |
| 42 | 103 | 25.0 | 229 | 7 | US-11-056-355B-12182 | Sequence 12182, A |
| 43 | 103 | 25.0 | 298 | 7 | US-11-056-355B-100544 | Sequence 100544, A |
| 44 | 103 | 25.0 | 298 | 7 | US-11-056-355B-111783 | Sequence 111783, A |
| 45 | 103 | 25.0 | 513 | 7 | US-11-056-355B-100543 | Sequence 100543, A |
| 46 | 103 | 25.0 | 513 | 7 | US-11-056-355B-111782 | Sequence 111782, A |
| 47 | 103 | 25.0 | 521 | 7 | US-11-056-355B-100542 | Sequence 100542, A |
| 48 | 103 | 25.0 | 521 | 7 | US-11-056-355B-111781 | Sequence 111781, A |
| 49 | 100 | 24.3 | 205 | 7 | US-11-056-355B-65080 | Sequence 65080, A |
| 50 | 100 | 24.3 | 233 | 7 | US-11-056-355B-65079 | Sequence 65079, A |
| 51 | 100 | 24.3 | 235 | 7 | US-11-056-355B-65078 | Sequence 65078, A |
| 52 | 100 | 24.3 | 237 | 7 | US-11-056-355B-13179 | Sequence 13179, A |
| 53 | 100 | 24.3 | 293 | 7 | US-11-056-355B-2204 | Sequence 2204, Ap |
| 54 | 100 | 24.3 | 294 | 7 | US-11-056-355B-13178 | Sequence 13178, A |
| 55 | 100 | 24.3 | 294 | 7 | US-11-056-355B-14163 | Sequence 14163, A |
| 56 | 100 | 24.3 | 504 | 7 | US-11-056-355B-14162 | Sequence 14162, A |
| 57 | 100 | 24.3 | 516 | 7 | US-11-056-355B-2203 | Sequence 2203, Ap |
| 58 | 99 | 24.0 | 205 | 7 | US-11-056-355B-51890 | Sequence 51890, A |
| 59 | 99 | 24.0 | 233 | 7 | US-11-056-355B-51889 | Sequence 51889, A |
| 60 | 99 | 24.0 | 235 | 7 | US-11-056-355B-51888 | Sequence 51888, A |
| 61 | 98 | 23.8 | 226 | 6 | US-10-449-902-45769 | Sequence 45769, A |
| 62 | 98 | 23.8 | 496 | 6 | US-10-449-902-43086 | Sequence 43086, A |
| 63 | 97 | 23.5 | 241 | 6 | US-10-953-349-28839 | Sequence 28839, A |
| 64 | 97 | 23.5 | 241 | 7 | US-11-056-355B-68617 | Sequence 68617, A |
| 65 | 97 | 23.5 | 266 | 6 | US-10-449-902-53649 | Sequence 53649, A |
| 66 | 97 | 23.5 | 273 | 6 | US-10-953-349-28838 | Sequence 28838, A |
| 67 | 97 | 23.5 | 273 | 7 | US-11-056-355B-68616 | Sequence 68616, A |
| 68 | 97 | 23.5 | 509 | 6 | US-10-449-902-33141 | Sequence 33141, A |
| 69 | 97 | 23.5 | 509 | 6 | US-10-449-902-43057 | Sequence 43057, A |
| 70 | 97 | 23.5 | 509 | 6 | US-10-449-902-43119 | Sequence 43119, A |
| 71 | 97 | 23.5 | 509 | 6 | US-10-449-902-44368 | Sequence 44368, A |
| 72 | 97 | 23.5 | 509 | 6 | US-10-449-902-45701 | Sequence 45701, A |
| 73 | 97 | 23.5 | 509 | 6 | US-10-449-902-56301 | Sequence 56301, A |
| 74 | 96 | 23.3 | 256 | 7 | US-11-056-355B-8801 | Sequence 8801, Ap |
| 75 | 96 | 23.3 | 258 | 7 | US-11-056-355B-16289 | Sequence 16289, A |
| 76 | 96 | 23.3 | 281 | 7 | US-11-056-355B-8800 | Sequence 8800, Ap |
| 77 | 96 | 23.3 | 473 | 7 | US-11-056-355B-16288 | Sequence 16288, A |
| 78 | 96 | 23.3 | 508 | 7 | US-11-056-355B-16287 | Sequence 16287, A |
| 79 | 94.5 | 22.9 | 370 | 6 | US-10-527-191-111 | Sequence 111, App |
| 80 | 92 | 22.3 | 380 | 7 | US-11-450-360-29 | Sequence 29, Appl |
| 81 | 92 | 22.3 | 450 | 6 | US-10-953-349-13719 | Sequence 13719, A |
| 82 | 92 | 22.3 | 451 | 6 | US-10-953-349-13718 | Sequence 13718, A |
| 83 | 92 | 22.3 | 508 | 6 | US-10-953-349-13717 | Sequence 13717, A |

| | | | | | | |
|-----|------|------|-----|---|----------------------|-------------------|
| 84 | 91 | 22.1 | 295 | 6 | US-10-953-349-8827 | Sequence 8827, Ap |
| 85 | 91 | 22.1 | 295 | 6 | US-10-953-349-10645 | Sequence 10645, A |
| 86 | 91 | 22.1 | 295 | 7 | US-11-056-355B-37269 | Sequence 37269, A |
| 87 | 91 | 22.1 | 295 | 7 | US-11-056-355B-43886 | Sequence 43886, A |
| 88 | 91 | 22.1 | 295 | 7 | US-11-056-355B-50072 | Sequence 50072, A |
| 89 | 91 | 22.1 | 381 | 7 | US-11-450-360-25 | Sequence 25, Appl |
| 90 | 91 | 22.1 | 433 | 6 | US-10-953-349-8826 | Sequence 8826, Ap |
| 91 | 91 | 22.1 | 433 | 6 | US-10-953-349-10644 | Sequence 10644, A |
| 92 | 91 | 22.1 | 433 | 7 | US-11-056-355B-37268 | Sequence 37268, A |
| 93 | 91 | 22.1 | 433 | 7 | US-11-056-355B-43885 | Sequence 43885, A |
| 94 | 91 | 22.1 | 433 | 7 | US-11-056-355B-50071 | Sequence 50071, A |
| 95 | 91 | 22.1 | 508 | 6 | US-10-953-349-8825 | Sequence 8825, Ap |
| 96 | 91 | 22.1 | 508 | 6 | US-10-953-349-10643 | Sequence 10643, A |
| 97 | 91 | 22.1 | 508 | 7 | US-11-056-355B-37267 | Sequence 37267, A |
| 98 | 91 | 22.1 | 508 | 7 | US-11-056-355B-43884 | Sequence 43884, A |
| 99 | 91 | 22.1 | 508 | 7 | US-11-056-355B-50070 | Sequence 50070, A |
| 100 | 89.5 | 21.7 | 118 | 7 | US-11-056-355B-12183 | Sequence 12183, A |
| 101 | 88 | 21.4 | 237 | 6 | US-10-449-902-31627 | Sequence 31627, A |
| 102 | 88 | 21.4 | 495 | 6 | US-10-449-902-44439 | Sequence 44439, A |
| 103 | 88 | 21.4 | 495 | 6 | US-10-449-902-50431 | Sequence 50431, A |
| 104 | 88 | 21.4 | 495 | 6 | US-10-449-902-53322 | Sequence 53322, A |
| 105 | 87 | 21.1 | 392 | 6 | US-10-953-349-36927 | Sequence 36927, A |
| 106 | 87 | 21.1 | 503 | 6 | US-10-953-349-36926 | Sequence 36926, A |
| 107 | 87 | 21.1 | 525 | 6 | US-10-953-349-36925 | Sequence 36925, A |
| 108 | 86.5 | 21.0 | 106 | 7 | US-11-056-355B-38056 | Sequence 38056, A |
| 109 | 86 | 20.9 | 233 | 7 | US-11-056-355B-7597 | Sequence 7597, Ap |
| 110 | 86 | 20.9 | 448 | 7 | US-11-056-355B-7596 | Sequence 7596, Ap |
| 111 | 85 | 20.6 | 413 | 6 | US-10-449-902-50838 | Sequence 50838, A |
| 112 | 85 | 20.6 | 522 | 6 | US-10-449-902-50452 | Sequence 50452, A |
| 113 | 80.5 | 19.5 | 78 | 7 | US-11-368-086-64 | Sequence 64, Appl |
| 114 | 79.5 | 19.3 | 379 | 7 | US-11-450-360-26 | Sequence 26, Appl |

GenCore version 5.1.9

Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:17:40 ; Search time 6.88742 Seconds
 (without alignments)
 1117.595 Million cell updates/sec

Title: US-10-801-517-2
 Perfect score: 412
 Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPELVCSMLHLCSG 80

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|--------|--------------------|
| 1 | 412 | 100.0 | 527 | 1 | SAHUP | saposin precursor |
| 2 | 343 | 83.3 | 80 | 2 | S21770 | saposin-C - bovine |
| 3 | 261 | 63.3 | 81 | 2 | A32026 | glucosylceramide b |
| 4 | 193 | 46.8 | 554 | 1 | A28716 | saposin precursor |
| 5 | 168 | 40.8 | 557 | 1 | JH0604 | saposin precursor |
| 6 | 158 | 38.3 | 965 | 2 | T00207 | Pl09 protein - sil |
| 7 | 106.5 | 25.8 | 217 | 2 | T48201 | hypothetical prote |
| 8 | 106 | 25.7 | 213 | 2 | T46069 | hypothetical prote |
| 9 | 106 | 25.7 | 428 | 2 | S47096 | cynarase (EC 3.4.2 |
| 10 | 106 | 25.7 | 474 | 2 | T12049 | cyprosin (EC 3.4.2 |
| 11 | 104 | 25.2 | 506 | 2 | F86253 | hypothetical prote |
| 12 | 103 | 25.0 | 292 | 2 | T14446 | aspartic proteinas |
| 13 | 103 | 25.0 | 322 | 2 | S41400 | aspartic proteinas |
| 14 | 103 | 25.0 | 433 | 2 | E96649 | hypothetical prote |
| 15 | 102.5 | 24.9 | 376 | 2 | S02766 | pulmonary surfacta |
| 16 | 102 | 24.8 | 506 | 2 | T07915 | probable aspartic |
| 17 | 102 | 24.8 | 509 | 2 | JC7272 | aspartic proteinas |
| 18 | 100 | 24.3 | 513 | 2 | T11686 | aspartic proteinas |
| 19 | 99.5 | 24.2 | 103 | 2 | D89567 | protein T08A9.8 [i |
| 20 | 99.5 | 24.2 | 363 | 2 | A29072 | pulmonary surfacta |
| 21 | 99 | 24.0 | 575 | 1 | A40292 | acyloxyacyl hydrol |
| 22 | 98 | 23.8 | 496 | 2 | JS0732 | aspartic proteinas |

| | | | | | | |
|----|------|------|-----|---|--------|--------------------|
| 23 | 97 | 23.5 | 508 | 2 | S19697 | aspartic proteinas |
| 24 | 97 | 23.5 | 509 | 2 | S66516 | oryzasin (EC 3.4.2 |
| 25 | 97 | 23.5 | 513 | 2 | T09739 | aspartic endopepti |
| 26 | 96.5 | 23.4 | 101 | 1 | S49145 | amoebapore C precu |
| 27 | 95 | 23.1 | 79 | 1 | LNPG1 | pulmonary surfacta |
| 28 | 95 | 23.1 | 369 | 2 | I46531 | surfactant protein |
| 29 | 92 | 22.3 | 509 | 2 | S49349 | cyprosin (EC 3.4.2 |
| 30 | 91 | 22.1 | 370 | 1 | LNRRBB | pulmonary surfacta |
| 31 | 91 | 22.1 | 381 | 1 | LNHUB | pulmonary surfacta |
| 32 | 91 | 22.1 | 508 | 2 | D85056 | probable aspartic |
| 33 | 90.5 | 22.0 | 96 | 1 | S49144 | amoebapore B precu |
| 34 | 90.5 | 22.0 | 98 | 1 | S25283 | amoebapore A precu |
| 35 | 89.5 | 21.7 | 205 | 2 | B89567 | protein T08A9.7 [i |
| 36 | 89 | 21.6 | 314 | 2 | T15674 | hypothetical prote |
| 37 | 87 | 21.1 | 195 | 2 | T15676 | hypothetical prote |
| 38 | 84.5 | 20.5 | 129 | 2 | S55044 | NK-lysin protein - |
| 39 | 82.5 | 20.0 | 280 | 2 | PC4080 | aspartic proteinas |
| 40 | 81.5 | 19.8 | 223 | 2 | E89567 | protein T08A9.9 [i |
| 41 | 79 | 19.2 | 650 | 2 | T00617 | endostyle-specific |
| 42 | 78.5 | 19.1 | 74 | 2 | C89567 | protein T08A9.10 [|
| 43 | 78 | 18.9 | 506 | 2 | S71591 | aspartic proteinas |
| 44 | 77.5 | 18.8 | 572 | 2 | T27869 | sphingomyelin phos |
| 45 | 76 | 18.4 | 306 | 2 | T09915 | hypothetical prote |

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2006, 11:17:37 ; Search time 23.4437 Seconds
(without alignments)
3156.550 Million cell updates/sec

Title: US-10-801-517-2
Perfect score: 412
Sequence: 1 SDVYCEVCEFLVKEVTKLID.....ILLEEVSPELVCSMLHLCSG 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|----------------|--------------------|
| 1 | 412 | 100.0 | 452 | 2 Q5R406_PONPY | Q5r406 pongo pygma |
| 2 | 412 | 100.0 | 524 | 1 SAP_HUMAN | P07602 h proactiva |
| 3 | 412 | 100.0 | 524 | 2 Q53FJ5_HUMAN | Q53fj5 homo sapien |
| 4 | 412 | 100.0 | 524 | 2 Q5JQ36_HUMAN | Q5jq36 homo sapien |
| 5 | 412 | 100.0 | 527 | 2 Q5NVD5_PONPY | Q5nvd5 pongo pygma |
| 6 | 412 | 100.0 | 530 | 2 Q59EN5_HUMAN | Q59en5 homo sapien |
| 7 | 412 | 100.0 | 559 | 2 Q5JQ37_HUMAN | Q5jq37 homo sapien |
| 8 | 405 | 98.3 | 526 | 2 Q5R4U7_PONPY | Q5r4u7 pongo pygma |
| 9 | 397 | 96.4 | 497 | 2 Q4R590_MACFA | Q4r590 m brain cdn |
| 10 | 346 | 84.0 | 525 | 1 SAP_BOVIN | P26779 b proactiva |
| 11 | 261 | 63.3 | 81 | 1 SAP_CAVPO | P20097 cavia porce |
| 12 | 210 | 51.0 | 512 | 2 Q7SY70_XENLA | Q7sy70 xenopus lae |
| 13 | 207 | 50.2 | 550 | 2 Q4RQ38_TETNG | Q4rq38 tetraodon n |
| 14 | 205 | 49.8 | 520 | 2 Q6P3G7_BRARE | Q6p3g7 brachydanio |
| 15 | 205 | 49.8 | 520 | 2 Q6PH48_BRARE | Q6ph48 brachydanio |
| 16 | 205 | 49.8 | 520 | 2 Q8UVZ4_BRARE | Q8uvz4 brachydanio |
| 17 | 205 | 49.8 | 522 | 2 Q9DG82_BRARE | Q9dg82 brachydanio |
| 18 | 203 | 49.3 | 518 | 1 SAP_CHICK | O13035 gallus gall |
| 19 | 193 | 46.8 | 518 | 2 Q642S6_XENLA | Q642s6 xenopus lae |
| 20 | 193 | 46.8 | 553 | 2 Q6P7A4_RAT | Q6p7a4 rattus norv |
| 21 | 193 | 46.8 | 554 | 1 SAP_RAT | P10960 rattus norv |
| 22 | 174 | 42.2 | 554 | 2 Q3TKB2_MOUSE | Q3tkb2 mus musculu |
| 23 | 174 | 42.2 | 554 | 2 Q3TKK3_MOUSE | Q3tkk3 mus musculu |
| 24 | 171 | 41.5 | 200 | 2 Q75K05_DICDI | Q75k05 dictyosteli |

| | | | | | | | | |
|----|-----|------|-----|---|--------------|--------|-------------|-----------|
| 25 | 169 | 41.0 | 527 | 2 | Q3TWM9_MOUSE | Q3twm9 | mus | musculu |
| 26 | 169 | 41.0 | 545 | 2 | Q3UAS4_MOUSE | Q3uas4 | m | bone marr |
| 27 | 169 | 41.0 | 551 | 2 | Q3UE29_MOUSE | Q3ue29 | mus | musculu |
| 28 | 169 | 41.0 | 553 | 2 | Q3TXJ0_MOUSE | Q3txj0 | m | osteoclas |
| 29 | 169 | 41.0 | 554 | 2 | Q3TID4_MOUSE | Q3tid4 | mus | musculu |
| 30 | 169 | 41.0 | 554 | 2 | Q3TIT5_MOUSE | Q3tit5 | mus | musculu |
| 31 | 169 | 41.0 | 554 | 2 | Q3TWE9_MOUSE | Q3twe9 | mus | musculu |
| 32 | 169 | 41.0 | 554 | 2 | Q3TWF9_MOUSE | Q3twf9 | mus | musculu |
| 33 | 169 | 41.0 | 554 | 2 | Q3TXP9_MOUSE | Q3txp9 | mus | musculu |
| 34 | 169 | 41.0 | 554 | 2 | Q3U5W2_MOUSE | Q3u5w2 | mus | musculu |
| 35 | 169 | 41.0 | 554 | 2 | Q3U825_MOUSE | Q3u825 | mus | musculu |
| 36 | 169 | 41.0 | 554 | 2 | Q3U897_MOUSE | Q3u897 | mus | musculu |
| 37 | 169 | 41.0 | 554 | 2 | Q3U8C4_MOUSE | Q3u8c4 | mus | musculu |
| 38 | 169 | 41.0 | 554 | 2 | Q8BFQ1_MOUSE | Q8bfq1 | m | 2 days ne |
| 39 | 169 | 41.0 | 557 | 1 | SAP_MOUSE | Q61207 | mus | musculu |
| 40 | 169 | 41.0 | 557 | 2 | Q3UFE8_MOUSE | Q3ufe8 | mus | musculu |
| 41 | 166 | 40.3 | 554 | 2 | Q3TWL8_MOUSE | Q3twl8 | mus | musculu |
| 42 | 164 | 39.8 | 522 | 2 | Q54Q68_DICDI | Q54q68 | dictyosteli | |
| 43 | 163 | 39.6 | 336 | 2 | Q54LG3_DICDI | Q54lg3 | dictyosteli | |
| 44 | 158 | 38.3 | 965 | 2 | O15997_BOMMO | O15997 | bombyx | mori |
| 45 | 155 | 37.6 | 245 | 2 | Q5ZL62_CHICK | Q5zl62 | gallus | gall |